Untitled Title: US- 10- 578- 672**A**- 1 Perfect score: 191 Sequence: 1 ggt gt ggaggt gt t caaagg. gacact aaat t gt ggat aat 191 RESULT 5 AAS69177 I D AAS69177 standard; cDNA; 1431 BP. XX AC AAS69177; XX DT 13-FEB-2002 (first entry) XX DE DNA encoding novel human diagnostic protein #4981. XX KW Human; chromosome mapping; gene mapping; gene therapy; forensic; food supplement; medical imaging; diagnostic; genetic disorder; ss. Homo sapiens. WO200175067- A2. 11- OCT- 2001. 30-MAR-2001; 2001WO-US008631. 31- MAR- 2000: 2000US- 00540217. 23- AUG- 2000; 2000US- 00649167. XX PA (HYSE-) HYSEQ INC. XX Pl Drmanac RT, Liu C, Tang YT; WPI; 2001-639362/73. P-PSDB; ABG04990. New isolated polynucleotide and encoded polypeptides, useful in diagnostics, forensics, gene mapping, identification of mutations responsible for genetic disorders or other traits and to assess bi odi versity. Claim 1; SEQ ID NO 4981; 103pp; English. The invention relates to isolated polynucleotide (I) and polypeptide (II) sequences. (I) is useful as hybridisation probes, polymerase chain reaction (PCR) primers, oligomers, and for chromosome and gene mapping, and in recombinant production of (II). The polynucleotides are also used in diagnostics as expressed sequence tags for identifying expressed genes. (I) is useful in gene therapy techniques to restore normal activity of (II) or to treat disease states involving (II). (II) is useful for generating antibodies against it, detecting or quantitating a polypeptide in tissue, as molecular weight markers and as a food supplement. (II) and its binding partners are useful in medical imaging of sites expressing (II). (I) and (II) are useful for treating disorders involving aberrant protein expression or biological activity. polypeptide and polynucleotide sequences have applications in diagnostics, forensics, gene mapping, identification of mutations responsible for genetic disorders or other traits to assess biodiversity and to produce other types of data and products dependent on DNA and am no acid sequences. AAS64197-AAS94564 represent novel human diagnostic coding sequences of the invention. Note: The sequence data for this patent did not appear in the printed specification, but was obtained in

Page 1

electronic format directly from WPO at ftp. wipo. int/pub/published_pct_sequences

Untitled

```
XX
SQ
    Sequence 1431 BP; 391 A; 346 C; 383 G; 311 T; 0 U; 0 Other;
 Query Match
Best Local Similarity
                                Score 158.6; DB 5; Length 1431; Pred. No. 2.4e-36;
                         83.0%
                         89.9%
 Mat ches
          170; Conservative
                                0; M smat ches
                                                     Indel s
                                                                           0;
                                                19;
                                                               0;
                                                                   Gaps
           3 TGTQGAQGTGTTCAAAQQCATTGACAATQQGACTCAGAAAGTAGTQQCCATAAAAATCAT 62
Qy
                 183 TGGAGAGGTGTTCAAAGGCATTGACAATCGGACTCAGAAAGTGGTTGCCATAAAGATCAT 242
Db
          63 TGACCTGGAGGAGGAGAGATGAGATGAGGACATTCACCAGGAAATCACAGTGCTGAG 122
Qy
         Db
Qy
         123 TCAGTGTGACAGTCCCTACGTAACCAAATATTACCGATCCTACCTGAAGGACACTAAATT 182
         303 TCAGTGTGACAGTCCATATGTAACCAAATATTATGGATCCTATCTGAAGGATACAAAATT 362
Db
         183 GTGGATAAT 191
Qy
              Db
         363 ATGGATAAT 371
               US-10-578-672A-1
Title:
Perfect score:
               191
Sequence:
               1 ggt gt ggaggt gt t caaagg. . . . . . . . . gacact aaat t gt ggat aat 191
RESULT 37
ACH38568
    ACH38568 standard; cDNA; 472 BP.
XX
AC
    ACH38568;
XX
13- CCT- 2003 (first entry)
    Human endothelial cell cDNA #6701.
    Human; ss; sequencing by hybridisation; SBH; expressed sequence tag; EST;
    genome mapping; biodiversity; genetic disorder.
    Homo sapi ens.
    US2003073623-A1.
    17- APR- 2003.
    30-JUL-2001; 2001US-00918995.
    30-JUL-2001; 2001US-00918995.
            DRMANAC R T.
     DRMA()
     LABA/ )
            LABAT I
PA
     STAC/ )
            STACHE- CRAIN B.
     (DICK/)
PΑ
            DICKSON M.C.
     (JONE/) JONES L W
PΑ
XX
РΙ
                                           Dickson MC, Jones LW
     Drmanac RT, Labat I, Stache-Orain B,
XX
```

Untitled

DR WPI; 2003-615964/58. New polynucleotide sequences obtained from various cDNA libraries, useful as hybridization probes, as oligomers for PCR, for chromosome and gene mapping, in the recombinant production of protein, or in generating antisense DNA or RNA. Claim 1; SEQ ID NO 25780; 44pp; English. The invention relates to an isolated polynucleotide comprising any one of 38043 cDNA sequences, appearing as ACH12789-ACH50831, whose sequence was determined by the technique of SBH (sequencing by hybridisation). Also included is a purified polypeptide comprising a sequence corresponding to a reading frame of the novel polynucleotide. The nucleic acid sequences are useful in diagnostics as expressed sequence tags (EST) for identifying expressed genes or for physical mapping of the human genome, in forensičs, in assesšing biodiversities, or in identifying mutations responsible for genetic disorders and other traits. The nucleotide sequences are also useful as hybridisation probes, as oligomers for PCR, for chromosome and gene mapping, in the recombinant production of protein, or in generating antisense DNA or RNA. The purified polypeptide is useful for generating antibodies specific for it. The present sequence is one of the 38043 isolated cDNAV EST sequences. Note: The sequence data for this patent did not form part of the printed specification, but was obtained in electronic format directly from USPTO at seqdat a. uspt o. gov/sequence. ht ml ?Docl D=20030073623 Sequence 472 BP; 149 A; 91 C; 119 G; 110 T; 0 U; 3 Other; 16.8% Score 32; DB 10; Length 472; 100.0% Pred. No. 6.6e-06; Query Match Best Local Similarity 0; M smatches Mat ches 32; Conservative Indels Gaps 0; Qy 106 GAAATCACAGTGCTGAGTCAGTGTGACAGTCC 137

178 GAAATCACAGTGCTGAGTCAGTGTGACAGTCC 209

Db